

SEQUENCE LISTING

<110> KIMCHI, Adi
 MCINNIS A., Patricia
 YEDA RESEARCH AND DEVELOPMENT COMPANY LTD.

<120> DAP-KINASE RELATED PROTEIN

<130> KIMCHI2A

<140> 00

<141> 1999-06-15

<150> 60/089,294

<151> 1998-06-15

<160> 14

<170> PatentIn Ver. 2.0

<210> 1

<211> 1742

<212> DNA

<213> Human

<220>

<221> CDS

<222> (62)..(1141)

<400> 1

gaccgcggca gctcagcctc ccgccgattg tatgttccag gcctcaatga ggagtccaaa 60

c atg gag cca ttc aag cag cag aag gtg gag gac ttt tat gac atc gga 109 Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly 1 5 10

gag gag ctg ggg agt ggc cag ttt gcc atc gtg aag aag tgc cgg gag 157 Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu 20 25 30

aag agc acg ggg ctt gag tat gca gcc aag ttc atc aag aag cgg cag 205 Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln 35 40 45

agc cgg gcg agc cgg cgc ggt gtg agc cgg gag gag atc gag cgg gag 255 Ser Arg Ala Ser Arg Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu 50 55 60

•	•															
gt	gago	ato	ctg	cgg	cag	gtg	ctg	cac	cac	aat	gtc	atc	acg	ctg	cac	301
Va	l Sei	: Ile	e Leu	Arg	Gln	Val	Leu	His	His	Asn	Val	Ile	Thr	Leu	His	
6	5				70					75					80	-
ga	gto	: tat	gag	aac	cgc	acc	gac	gtg	gtg	cac	atc	ctt	gag	cta	gtg	349
				Asn												
	•	•		85	_		_	•	90					95		
·													. •		-	
tc	t aga	a aa	a gag	ctc	ttc	gat	ttc	ctq.	qcc	caq	aaq	gag	tca	ctg	agt	397
				Leu												
			100					105			•		110			
٠ حـء	~ ~~	T (T2)		acc	acc	ttc	att	aac	cag	atc	cta	gat	aaa	ata	aac	445
_				Thr												
GI	u GI			1111	261	FIIC		шуз	GIII	110	200	125	U _1	•	• • • • • • • • • • • • • • • • • • • •	
		11!	•				120					123				
				224			~~+			~a+	ctc	224	cca	722	220	493
				aag												400
ту			s Thi	Lys	ьys		Ala	nis	Pne	ASP		пуэ	PIO	GIU	ASII	
	13	נ				135					140					
							- 4- 4-									E 4 1
				gac	_											541
		t Le	ı Lev	Asp		Asn	IIe	Pro	TTE		HIS	TTE	ьys	Leu		
14	5				150					155					160	
																500
_			_	gct												589
As	p Ph	e Gl	y Lei	Ala		GIu	IIe	GIU		GTA	vaı	GIU	Pne		Asn	
				165					170					175		
									•							
				ccg												637
Il	e Ph	e Gl	_	Pro	Glu	Phe	Val		Pro	Glu	Ile	Val		Tyr	GIU	
			180)				185					190			
				gag												685
Pr	o Le	u Gl	y Lei	ı Glu	Ala	Asp	Met	Trp	Ser	Ile	Gly			Thr	Tyr	
		19	5				200					205				
			_	gga												733
Il	e Le	u Le	u Sei	Gly	r Ala	Ser	Pro	Phe	Leu	Gly	' Asp	Thr	Lys	Gln	Glu	
	21	0				215					220					
				ato												781
Th	r Le	u Al	a Ası	ı Ile	: Thr	Ser	Val	Ser	Tyr	Asp	Phe	Asp	Glu	Glu	Phe	
22	5				230)				235	;				240	
tt	c ag	с са	t ac	gago	gag	ctg	gcc	: aag	gac	ttt	att	cgg	aag	ctt	ctg	829
				r Ser												
				245					250					255		

	•														626	877
	aaa Lys															677
	tgg Trp															925
	gtg Val 290															973
	aag Lys															1021
	ctg Leu															1069
	gag Glu															1117
	cgg Arg		Arg						ctgg	cct	gacc	tgca	gt g	gccg	ccagg	1171
gag	gttt	aaa	ccca	gcgg	gg c	tccc	ttct	g tg	caga	cttt	tgg	accc	agc	tcag	caccag	1231
cad	:ccgg	gcg	tcct	gagc	ac t	ttgc	aaga	g ag	atgg	gccc	aag	gaat	tca	gaag	agcttg	1291
cag	gcaa	gcc	agga	gacc	ct g	ggag	ctgt	g gc	tgtc	ttct	gtg	gagg	agg	ctcc	agcatt	1351
cc	caaag	ctc	ttaa	ttct	.cc a	taaa	atgg	g ct	ttcc	tctg	tct	gcca	tcc	tcag	agtctg	1411
999	gtggg	agt	gtgg	actt	ag g	aaaa	caat	a ta	aagg	acat	cct	cato	atc	acgg	ggtgaa	1471
gg	caga	gta	aggo	agco	ett c	ttca	.cagg	c tg	aggg	ggtt	cag	raacc	agc	ctgg	ccaaaa	1531
at	tacac	cag	agag	racag	rag t	cctc	ccca	t tg	ggaa	.cagg	gtg	gattg	ragg	aaag	tgaacc	1591
tt	gaata	rtga	ggga	ccaa	itc o	tgtg	acct	.c cc	agaa	ccat	gga	agco	agg	acgt	cagget	1651
ga			tcag				rcago	c ca	ittgo	tggc	ccg	gecat	gtt	gtaa	ttttgc	1711

<210> 2

<211> 360

<212> PRT

<213> Human

<400> 2

Met Glu Pro Phe Lys Gln Gln Lys Val Glu Asp Phe Tyr Asp Ile Gly
1 5 10 15

Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Lys Lys Cys Arg Glu 20 25 30

Lys Ser Thr Gly Leu Glu Tyr Ala Ala Lys Phe Ile Lys Lys Arg Gln 35 40 45

Ser Arg Ala Ser Arg Gly Val Ser Arg Glu Glu Ile Glu Arg Glu
50 55 60

.Val Ser Ile Leu Arg Gln Val Leu His His Asn Val Ile Thr Leu His 65 70 75 80

Asp Val Tyr Glu Asn Arg Thr Asp Val Val His Ile Leu Glu Leu Val 85 90 95

Ser Gly Glu Leu Phe Asp Phe Leu Ala Gln Lys Glu Ser Leu Ser 100 105 110

Glu Glu Glu Ala Thr Ser Phe Ile Lys Gln Ile Leu Asp Gly Val Asn 115 120 125

Tyr Leu His Thr Lys Lys Ile Ala His Phe Asp Leu Lys Pro Glu Asn 130 135 140

Ile Met Leu Leu Asp Lys Asn Ile Pro Ile Pro His Ile Lys Leu Ile 145 150 155 160

Asp Phe Gly Leu Ala His Glu Ile Glu Asp Gly Val Glu Phe Lys Asn 165 170 175

Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile Val Asn Tyr Glu 180 185 190

Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly Val Ile Thr Tyr 195 200 205

Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln Glu 210 215 220

Thr Leu Ala Asn Ile Thr Ser Val Ser Tyr Asp Phe Asp Glu Glu Phe 225 230 235 240

Phe Ser His Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu Leu 245 250 255

Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg His
260 265 270

Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg Glu 275 280 285

Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg 290 295 300

Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg 305 310 315 320

Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg Asn 325 330 335

Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu His 340 345 350

Pro Arg Arg Ser Ser Thr Ser 355 360

<210> 3 <211> 263 <212> PRT

<213> Human

<400> 3

Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Val Val Lys
1 5 10 15

Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln Tyr Ala Ala Lys Phe Ile 20 25 30

Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg Gly Val Ser Arg Glu Asp 35 40 45

Ile Glu Arg Glu Val Ser Ile Leu Lys Glu Ile Gln His Pro Asn Val 50 55 60

Ile Thr Leu His Glu Val Tyr Glu Asn Lys Thr Asp Val Ile Leu Ile

80

Leu Glu Leu Val Ala Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys 85 90 95

Glu Ser Leu Thr Glu Glu Glu Ala Thr Glu Phe Leu Lys Gln Ile Leu 100 105 110

Asn Gly Val Tyr Tyr Leu His Ser Leu Gln Ile Ala His Phe Asp Leu 115 120 125

Lys Pro Glu Asn Ile Met Leu Leu Asp Arg Asn Val Pro Lys Pro Arg 130 135 140

Ile Lys Ile Ile Asp Phe Gly Leu Ala His Lys Ile Asp Phe Gly Asn 145 150 155 160

Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile 165 170 175

Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
180 185 190

Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp 195 200 205

Thr Lys Gln Glu Thr Leu Ala Asn Val Ser Ala Val Asn Tyr Glu Phe 210 215 220

Glu Asp Glu Tyr Phe Ser Asn Thr Ser Ala Leu Ala Lys Asp Phe Ile 225 230 235 240

Arg Arg Leu Leu Val Lys Asp Pro Lys Lys Arg Met Thr Ile Gln Asp 245 250 255

Ser Leu Gln His Pro Trp Ile 260

<210> 4

<211> 263

<212> PRT

<213> Human

<400> 4

Tyr Glu Met Gly Glu Glu Leu Gly Ser Gly Gln Phe Ala Ile Val Arg
1 5 10 15

Lys Cys Arg Gln Lys Gly Thr Gly Lys Glu Tyr Ala Ala Lys Phe Ile 20 25 30

Lys Lys Arg Arg Leu Ser Ser Ser Arg Gly Val Ser Arg Glu Glu
35 40 45

Ile Glu Arg Glu Val Asn Ile Leu Arg Glu Ile Arg His Pro Asn Ile 50 55 60

. Ile Thr Leu His Asp Ile Phe Glu Asn Lys Thr Asp Val Val Leu Ile 65 70 75 80

Leu Glu Leu Val Ser Gly Gly Glu Leu Phe Asp Phe Leu Ala Glu Lys
85 90 95

Glu Ser Leu Thr Glu Asp Glu Ala Thr Gln Phe Leu Lys Gln Ile Leu 100 105 110

Asp Gly Val His Tyr Leu His Ser Lys Arg Ile Ala His Phe Asp Leu 115 120 125

Lys Pro Glu Asn Ile Met Leu Leu Asn Lys Asn Val Pro Asn Pro Arg 130 135 140

Ile Lys Leu Ile Asp Phe Gly Ile Ala His Lys Ile Glu Ala Gly Asn 145 150 155 160

Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu Phe Val Ala Pro Glu Ile 165 170 175

Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala Asp Met Trp Ser Ile Gly
180 185 190

Val Ile Thr Tyr Ile Leu Leu Ser Gly Ala Ser Pro Phe Leu Gly Glu 195 200 205

Thr Lys Gln Glu Thr Leu Thr Asn Ile Ser Ala Val Asn Tyr Asp Phe 210 215 220

Asp Glu Glu Tyr Phe Ser Asn Thr Ser Glu Leu Ala Lys Asp Phe Ile 225 230 235 240

Arg Arg Leu Leu Val Lys Asp Pro Lys Arg Arg Met Thr Ile Ala Gln 245 250 255

Ser Leu Glu His Ser Trp Ile 260 <210> 5

<211> 261

<212> PRT

<213> Human

<400> 5

Leu Cys Pro Gly Arg Glu Leu Gly Arg Gly Lys Phe Ala Val Val Arg
1 5 10 15

Lys Cys Ile Lys Lys Asp Ser Gly Lys Glu Phe Ala Ala Lys Phe Met
20 25 30

Arg Lys Arg Arg Lys Gly Gln Asp Cys Arg Met Glu Ile Ile His Glu 35 40 45

Ile Ala Val Leu Glu Leu Ala Gln Asp Asn Pro Trp Val Ile Asn Leu5055

His Glu Val Tyr Glu Thr Ala Ser Glu Met Ile Leu Val Leu Glu Tyr
65 70 75 80

Ala Ala Gly Gly Glu Ile Phe Asp Gln Cys Val Ala Asp Arg Glu Glu 85 90 95

Ala Phe Lys Glu Lys Asp Val Gln Arg Leu Met Arg Gln Ile Leu Glu 100 105 110

Gly Val His Phe Leu His Thr Arg Asp Val Val His Leu Asp Leu Lys
115 120 125

Pro Gln Asn Ile Leu Leu Thr Ser Glu Ser Pro Leu Gly Asp Ile Lys 130 135 140

Ile Val Asp Phe Gly Leu Ser Arg Ile Leu Lys Asn Ser Glu Glu Leu 145 150 155 160

Arg Glu Ile Met Gly Thr Pro Glu Tyr Val Ala Pro Glu Ile Leu Ser 165 170 175

Tyr Asp Pro Ile Ser Met Ala Thr Asp Met Trp Ser Ile Gly Val Leu 180 185 190

Thr Tyr Val Met Leu Thr Gly Ile Ser Pro Phe Leu Gly Asn Asp Lys
195 200 205

Gln Glu Thr Phe Leu Asn Ile Ser Gln Met Asn Leu Ser Tyr Ser Glu 210 215 220 Glu Glu Phe Asp Val Leu Ser Glu Ser Ala Val Asp Phe Ile Arg Thr 225 230 235 240

Leu Leu Val Lys Lys Pro Glu Asp Arg Ala Thr Ala Glu Glu Cys Leu 245 250 255

Lys His Pro Trp Leu 260

<210> 6

<211> 261

<212> PRT

<213> Human

<400> 6

Ile Leu Thr Ser Lys Glu Leu Gly Arg Gly Lys Phe Ala Val Val Arg

1 5 10 15

Gln Cys Ile Ser Lys Ser Thr Gly Gln Glu Tyr Ala Ala Lys Phe Leu 20 25 30

Lys Lys Arg Arg Gly Gln Asp Cys Arg Ala Glu Ile Leu His Glu 35 40 45

Ile Ala Val Leu Glu Leu Ala Lys Ser Cys Pro Arg Val Ile Asn Leu 50 55 60

His Glu Val Tyr Glu Asn Thr Ser Glu Ile Ile Leu Ile Leu Glu Tyr
65 70 75 80

Ala Ala Gly Gly Glu Ile Phe Ser Leu Cys Leu Pro Glu Leu Ala Glu 85 90 95

Met Val Ser Glu Asn Asp Val Ile Arg Leu Ile Lys Gln Ile Leu Glu 100 105 110

Gly Val Tyr Tyr Leu His Gln Asn Asn Ile Val His Leu Asp Leu Lys 115 120 125

Pro Gln Asn Ile Leu Leu Ser Ser Ile Tyr Pro Leu Gly Asp Ile Lys
130
135
140

Ile Val Asp Phe Gly Met Ser Arg Lys Ile Gly His Ala Cys Glu Leu 145 150 155 160

Arg Glu Ile Met Gly Thr Pro Glu Tyr Leu Ala Pro Glu Ile Leu Asn

165 170 175

Tyr Asp Pro Ile Thr Thr Ala Thr Asp Met Trp Asn Ile Gly Ile Ile 180 185 190

Ala Tyr Met Leu Leu Thr His Thr Ser Pro Phe Val Gly Glu Asp Asn 195 200 205

Gln Glu Thr Tyr Leu Asn Ile Ser Gln Val Asn Val Asp Tyr Ser Glu 210 215 220

Glu Thr Phe Ser Ser Val Ser Gln Leu Ala Thr Asp Phe Ile Gln Ser 225 230 235 240

Leu Leu Val Lys Asn Pro Glu Lys Arg Pro Thr Ala Glu Ile Cys Leu . 245 250 255

Ser His Ser Trp Leu 260

<210> 7

<211> 29

<212> PRT

<213> Human

<400> 7

Asn Met Glu Lys Phe Lys Lys Phe Ala Ala Arg Lys Lys Trp Lys Gln 1 5 10 15

Ser Val Arg Leu Ile Ser Leu Cys Gln Arg Leu Ser Arg 20 25

<210> 8

<211> 29

<212> PRT

<213> Human

<400> 8

Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu

1 5 10 15

Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr Arg 20 25

<210> 9

<211> 29

<212> PRT

<213> Human -

<400> 9

Thr Cys Asp Cys Leu Lys Lys Leu Asn Ala Arg Arg Lys Leu Lys Gly

1 10 15

Ala Ile Leu Thr Thr Met Leu Ala Thr Arg Asn Phe Ser
. 20 25

<210> 10

<211> 28

<212> PRT

<213> Human

<400> 10

Val Ser Glu Gln Ile Lys Lys Asn Phe Ala Lys Ser Lys Trp Lys Gln

1 10 15

Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
20 25

<210> 11

<211> 32

<212> PRT

<213> Human

<400> 11

Met Asp Thr Ala Gln Lys Lys Leu Gln Glu Phe Asn Ala Arg Arg Lys

1 5 10 15

Leu Lys Ala Ala Val Lys Ala Val Val Ala Ser Ser Arg Leu Gly Ser 20 25 30

<210> 12

<211> 28

<212> PRT

<213> Human

<400> 12

Gly Glu Asp Ser Gly Arg Lys Pro Glu Arg Arg Arg Leu Lys Thr Thr





15

5 10

Arg Leu Lys Glu Tyr Thr Ile Lys Ser His Ser Ser 20 25

<210> 13

<211> 20

<212> DNA

<213> Human

<400> 13

ggccggatga ggacctgagg

20

<210> 14

<211> 21

<212> DNA

<213> Human

<400> 14

tccacatccc accccagact c

21